

Application No: 10/782,570  
Amendment Dated: May 12, 2006  
Reply to Office Action of February 14, 2006  
REPLACEMENT SHEET

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axmi007      -----MNQNNNNEYEIIDSKNLSYPSNRNIDHSRYPYTNNPNQPLQNTNYKEWLNMCQGN 55
cry1Aa      -----MDNNPNINECIPYN---CLSNPE-----VEVL 24
cry1Ac      -----MDNNPNINECIPYN---CLSNPE-----VEVL 24
cry1Ia      -----MKLKNQDKHQSFSSNAKVDKISTDS---LKNETDIELQINIHEDCLKMSEYE 49
cry3Aa1     MIRKGGRRKMNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADN 60
cry3Ba      MIRMGGRRKMNNRSEYDTIKVTPNSELPTNHNQYPLADNPSTLEELNYKEFLRMTADN 60
cry4Aa      ---MNPYQNKNEYETLNASQKKLNISN--NYTRYPIENSPKQLLQSTNYKDWLNMCCQN 54
cry6Aa      -----
cry7Aa      -----MNLNLD--GYEDSNRTLNNSLNYP---TQKALSPSLKMNMYQDFLSITERE 47
cry8Aa      -----MSPNNQNEYEIIDATPSTSVSSDSNRYPFANEPTDALQNMNYKDYLKMSGGE 52
cry10Aa     ---MNPYQNKNEYEIFNAPSNGFSKSN--NYSRYPLANKPNQPLKNTNYKDWLNVCCQN 54
cry16Aa     ---MHYYGNRNEYDILNASSNDSNMSN--TYPRYPLANPQQDLMQNTNYKDWLNVCEGY 54
cry19Ba     ---MNSYQNKNEYEILDAKRNTCHMSN--CYPKYPLANDPQMYLRNTHYKDWINMCEEA 54
cry24Aa     ---MNQYQNKNEYEILESSQNNMMPN----RYPFADDPNAVMMKNGNYKDWVNECEGS 51

axmi007      TQYGDNFETFASADTIAAVSAGTIVSGTLLAGIGGLTSISGPIGIIIGAIISFGTLITVF 115
cry1Aa      G-----GERIETGYTPIDISLSLTQFLLEF-VPGAGFVLG-----LVDIIGWIF 68
cry1Ac      G-----GERIETGYTPIDISLSLTQFLLEF-VPGAGFVLG-----LVDIIGWIF 68
cry1Ia      N-----VEPFVS-ASTIQTGIGIAGKILGTLGVPPFAGQVAS-----LYSFILGEL 93
cry3Aa1     N-----TEALDSSTTKDVIQKGISVVGDLGVLGVPPFAGALVS-----FYTNFLNTI 107
cry3Ba      S-----TEVLDSSTVKDAVGTGISVVGQILGVGVPPFAGALTS-----FYQSFLNAI 107
cry4Aa      QQYGGDFETFIDSG---ELSAITIVVGTVLTGFGFTTPLG-----LALIGFGTLIPVL 104
cry6Aa      -----MIIDSKTTLPRHSLIHTIKLNSNKKYGPDMTN-----GNQFIIS 40
cry7Aa      Q-----PEALASGNTAINTVVSVTGATLSALGVPGASFITN-----FYLKIAGLL 92
cry8Aa      NP-ELFGNPETFIS-SSTIQTGIGIVGRILGALGVPPFASQIAS-----FYSFIVGQL 102
cry10Aa     QQYGNNAAGNFASSETIVGVSAIIVVGTMLGAFAPVLAAG-----IISFGTLPIF 106
cry16Aa     H-----IENPREASVRAGLGKGLGIVSTIVGFFGGSIIIDLTIG-----LFYQISELL 101
cry19Ba     S-----YASSGPSQL---FKVGSIVAKILG-----MIPEVGP-----LLSWMVSLF 93
cry24Aa     N-----ISPSPAAAITSKIVSIVLKTAKAVASSLAD-----SIKSSLG 90

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axmi007      WPAGEQDKTVWTQFIKMGEIFVDTPLTESIKQLKLQTLLEGFRQILQ---SYNTALDDWRK 172
cry1Aa      GPS--Q---WDAFPVQIEQLINQRIEEFARNQAISRLEGLSNLYQ---IYAESFREWEA 119
cry1Ac      GPS--Q---WDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQ---IYAESFREWEA 119
cry1Ia      WP---KGKNQWEIFMEHVVEIINQKISTYARNKALTDLKGLGDALA---VYHDSLESWVG 147
cry3Aa1     WPS--E--DPWKAFMEQVEALMDQKIADYAKNKALAEQGLQNNVE---DYVSALSSWQK 160
cry3Ba      WPS--DA-DPWKAFMAQVEVLIDKKIEEYAKSKALAEQGLQNNFE---DYVNALDSWKK 161
cry4Aa      FPAQDQS-NTWSDFITQTKNIKKIEASTYISNANKILNRSFNVIS---TYHNHLKTWE- 159
cry6Aa      KQE-----WATIGAYIQTGLGLPVNEQQRLRTHVNLSQDISIPSDFSQLYDVYCS---- 89
cry7Aa      WPE--NGKI-WDEFMTEVEALIDQKIEEYVRNKAIAELDGLGSALD---KYQKALADWLG 146
cry8Aa      WPS--KSVDIWGEIMERVEELVDQKIEKYVKDKALAEKGLGNALD---VYQQSLEDWLE 157
cry10Aa     WQGS DPA-NVWQDLLNIGGRPIQ-EIDKNIINVLTSIVTPIKNQLD---KYQEFFDKWEP 161
cry16Aa     WPEDDTQQYTQDIMNHVEDLIDKRITVIRGNAIRTLADLQKQVD---DYNWNLKKWKD 158
cry19Ba     WPTIEEKNTVWEDMIKYVANLLKQELTNDTLNRATSNLSGLNESLN---IYNRALAAWKQ 150
cry24Aa     ISKTITENNVSQVSMVQVHQIINRRIQETILDLGESSLNLGLVAIYNR---DYLGALEAWN 148

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Fig. 1A

Fig. 1B

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axmi007	REIYTTEINFDRPLYL-----EIQPNLAIMEYNLTRSGLRLFSFLDELIFYTKNETYG	396
cry1Aa	REIYTNPVLENFDGS-----FRG--MAQRIEQNIRQPHLMDILNSITIYTDVHRGF	313
cry1Ac	REIYTNPVLENFDGS-----FRG--SAQGIERSIRSPHLMDILNSITIYTDHARGY	313
cry1Ia	REVYTDAGTVHPHPSFTSTTWYNNNAPSFSFAIEAAVVRNPHLLDFLEQVTIYSLLS--R	350
cry3Aa1	RDVLTDPIVGVNNLR-----GYGTTFSNIEN-YIRKPHLFDYLHRIQFHTRFQPGY	358
cry3Ba	RDIFTDPIFTLNALQ-----EYGPTFSSNIEN-SIRKPHLFDYLRGIEFHTRLRPGY	359
cry4Aa	REIY-QVLNFEESPYK-----YYD--FOYQEDSLTRR-PHLFTWLDLSLNFYEKAQTP	376
cry6Aa	KELLEKVKNLKTTLER-----TIKAEQDLEKKVEYSFLLGPLLGFFVVEILEN	270
cry7Aa	REVYTDPVLSISNP-----DIGPSFSQMENTAIRTPLHVDYLDDELYIYTSKYKAF	342
cry8Aa	RDVYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVRPPHLFDILSSVEINTSRGGIT	362
cry10Aa	REVY---TNVNSDTRF-----TIT---ELENGLTRN-PTLFTWINQGRFYTRNSRDI	358
cry16Aa	REIYSDVINGEIIYGLM-----TPYFSFEKAESLYTRA-PHLFTWLKGFRTVNSISYW	357
cry19Ba	REIYSDVINDHVYGLM-----VPYISFEHAESLYTRR-PHAFTWLKGFRTVNSINSW	350
cry24Aa	RKIYTDVPGRTDSPSFG-DWTNTGRTLAFNDLEREVTDSPSLVKWLGDMTIYTGADSY	351
	...:	
axmi007	NRLVGIAN-RNRSTYATTGTEIIYGERTGPPTT-KTLIPFESYKVSIVTDRQVTPTSFPF	454
cry1Aa	N-----YWSGHQITASPVGFGSGPEFAFPLFGNAGNAAPP-VLVSLTGLGIFRTLSSP	364
cry1Ac	Y-----YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS	365
cry1Ia	WSNTQYMN-MWGGHKLEFRTIGGTNLISTQ---GSTNTSINPVTLPTSTRDVYRTESLA	405
cry3Aa1	YGNDSTFN--YWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQ--NLEFNGEKVYRAVANT	414
cry3Ba	SGKDSFN--YWSGNYVETRPSIGSNDITSPFYGDKSIEPIQ--KLSFDGQKVYRTIANT	415
cry4Aa	NNFFTSHY-NMFHYTLDNISQKSSVFGNHNVT-D-KLKSGLATNIYIFLLNVLISLDNKYL	434
cry6Aa	TAVQHIKN--QIDEIKKQLDSAQHDLDKIDVGIIGMLNSINTDIDNLYSQGQEAIVFQKL	328
cry7Aa	SHEIQPDLFYWSAHKVSFKKSEQSN-LYTTGIYKTSYGISS-GAYSFHGNDIYRTLAAP	400
cry8Aa	LNNDAYIN-YWSGHTLKYRRTADSTVYTA---NYGRITSEKNSFALEDKDFEINSTV	417
cry10Aa	LDPYDIFS-FTGNQMAFTHTDNRNIIWGAHVH-NIISQDTSKVFPFYRNKPIDKVEIVR	416
cry16Aa	TFLSGGQN-KYSYTN-NSSINEGSRGQDTEYGGTSSSTINIPSNYSVYNLWTENYIYIP	415
cry19Ba	TFLSGGEN-RYFLTHGEGTIYNGPFLGQDTEYGGTSSYIDISNNSIYNLWTKNYEWIYP	409
cry24Aa	RPTSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTAYEDPSTFISNILYDDIYKLDLRA	411
axmi007	N-IYFTINQIELYLNNSP--SNKLTYSAGGNLSNDKKTDFQFPVKKDKCPPII--NPNCL	509
cry1Aa	---LYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRTVDSLVDVIPPQDNSV	421
cry1Ac	---LYRRPFN-IGINNQQLSVLDGTEFAYG-TSSNLPSAVYRKSGTVDSLDEIPPQNNNV	420
cry1Ia	GLNLFLTQPVNGVPRVDFHWKFVTHPIASDNFYYPGYAGIG--TQLQDSENELPPEATGQ	463
cry3Aa1	NLAVWP-SAVYSGVTKEVFSQYNDQTDEASTQTYDSKRN-VGAV-SWDSIDQLPPETTDE	471
cry3Ba	DIAAFPDGKIYFGVTKVDFSQYDDQKNETSTQTYDSKRY-NGYLGAQDSIDQLPPETTDE	474
cry4Aa	N-DYNNISKMDFFITNGTRLLEKELTAGSGQITYDVNKNIFGLPILKRRENQG--NPTLF	491
cry6Aa	QGIWATIGAQIENLRTTSLQEVQDSDDADEIQIELEDASDAWLVAQEAR-----	379
cry7Aa	SVVVYPYTQN-YGVEQVEFYGVKGHVHYRGDNKYDL-----TYDSIDQLPPDGE--	448
cry8Aa	ANLANYQKAYGVPGSWFHMVKRGTSSTAYLYSKTHTALQGCTQVYESSDEIPLDRT-V	476
cry10Aa	HREYSIIYEMIFFSNSS---EVFRYSSNSTIENNYKRTDSYMIKPQTWKN-----	464
cry16Aa	WGDPVNITKMNFSVTDNN--SSKELIYGAHRTNKPVVRTDFDFTLNKEGTE-----L	465
cry19Ba	WTDPVNITKINFISITDNS--NSSEIYGAERMNKPTVRTDFNLLNRAGNG-----P	459
cry24Aa	AAVSTIQGAMDTTFGVSSSRFFDIRGNQLYQSNKPYPSLPITITFPGEESSE-----	464

Fig. 1C

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axmi007	PSYNSYSHILSQFSLFNYSYKIGLALNILYTGALGWTHSSVNRNNAISDKIITMIPAIGK	569
cry1Aa	PPRAGFSHRLSHVMTLSQAAG---AVYTLRAPTFWSQHRSAEFNNIIPSSQITQIPLTKS	478
cry1Ac	PPRQGFSHRLSHVSMFRSGFSNS-SVSIIRAPMFWSIHRSAEFNNIIASDSITQIPAVKG	479
cry1Ia	PNYESYSHRLSHIGLISASHVK--ALVYS-----WTHRSADRTNTIEPNSITQIPLVKA	515
cry3Aa1	PLEKGYSHQNLNYVMCFLMQGSR-----GTIPVLTWTHKSVDFFNMIDSKKITQLPLVKA	525
cry3Ba	PLEKAYSHQNLNAYECFLMQDRR-----GTIPFFTWTWTHRSVDFFNTIDAEDITQIPVKA	528
cry4Aa	PTYDNYSHILSFIKSLSIP----ATYKTQVYTFAWTHSSVDPKNTIYTHLTQIPAVKA	546
cry6Aa	-----FTLNAYSTNSRQNLPIINVISDSCNCST	406
cry7Aa	PIHEKYTHRLCHATAIFKSTP---DYDNATIPIFSWTHRSAEYNNRIYSDKITQIPAVKM	505
cry8Aa	PVAESYSHRLSHITSHSFSKNG--SAYYGSFPVFWTHTSADLNNTIYSDKITQIPAVKG	534
cry10Aa	---EEYGHTLSYIKTDNYIFS---VVRERRRVAFSWTHTSVDFFQNTIDLNDITQIHALKA	518
cry16Aa	AKYNDYNHILSYMLINGETFG-----QKRHGYSFAFTHSSVDPNNTIAANKITQIPVKA	520
cry19Ba	TTYNDYNHILSYMLINGETFG-----QKRHGYSFAFTHSSVDYNTIVDPKIVQIPAVKT	514
cry24Aa	GNANDYSHLLCDVKILQEDSSN-ICEGRSSLLSHAWTHASLDRNNTILPDEITQIPAVTA	523
	* : : :	
axmi007	NSLDTNSKVIEGPGHTGGNLVYLQSQGR-----LEITCRTPNSTQSYIIRLRYATNGA	622
cry1Aa	TNLGSGTSSVVKGPFGTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYASTTN	533
cry1Ac	NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP	538
cry1Ia	FNLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPF-----AQRYRVRIRYASTTD	570
cry3Aa1	YKLQSGASVVAGPRFTGGDIIQCTENG----SAATYVTP-DVSYSQKYRARIHYASTSQ	580
cry3Ba	YALSSGASIIIEGPGFTGGNLLFLKESN---SIKFKVTLNSAALLQRYRVRIRYASTTN	585
cry4Aa	NSLGTASKVVQGPFGHTGGDLIDFKDH-----FKITCQHSNFQOSYFIRIRYASNGS	597
cry6Aa	TNMTSNQYSNPTTNMTS-----NQYMSISHEYTSPLN	437
cry7Aa	YKLDDPSTVVVKGPFGTGGDLVKGSTGYIGDIKATVNSPL-----SQRYRVRVRYATNVS	560
cry8Aa	DMLYLGGSVVQGPFGTGGDILKRTNPSILGTFAVTVNGSL-----SQRYRVRIRYASTTD	589
cry10Aa	LKVSSDSKIVKGPFGHTGGDLVILKDSMD-----FRVRFLKN-VSRQYQVRIRYATNAP	570
cry16Aa	SSINGSISIEKGPFGTGGDLVKMRADSG-----LTMRFKAELLDKKYRVRIRYKCNYS	573
cry19Ba	NLVG--ANIIKGPFGHTGGDLLKLEYERF-----LSLRIK-LIASMTFRIRIRYASNIS	564
cry24Aa	YELRGNSSVVAGPGSTGGDLVKMSYHS-----VWSFKVYCSELKNYRVRIRYASHGN	575
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axmi007	GNTLPNISLTIPGVIGIPPQRLNNTFSGTNYNNLQYGDGFGYFQFPSTVTLPLNR--NIPF	680
cry1Aa	LQFHTSIDGRPINQGNFS-----ATMSSGSNLQSGSFRTVGFTTTFNFNSNGS---SVF	583
cry1Ac	IHLNVNWNSSIFSNTVP-----ATATSLDNLQSSDFGYFESANAFTSSLGN-----	585
cry1Ia	LQFHTSINGKAINQGNFS-----ATMNRGEDLDYKTFRTVGFTTTFPSFLDVQ---STF	620
cry3Aa1	ITFTLSLDGAPFNQYYFD-----KTINKGDTLTYSFNLASFSTPFELSG-----NNL	628
cry3Ba	LRLFVQNSNNDLVIYIN-----KTMNIDGDLTYQTFDFATSNSNMGFSGDT---NDF	635
cry4Aa	ANTRAVINLSIPGVAELG-MALNPTFSGTDYTNLKYKDFQYLEFSNEVKFAPNQ--NISL	654
cry6Aa	NFMLSRNSNLEYKCPENN-----FMIYWYNNSDWYNNSDWYNN-----	475
cry7Aa	GQFNVIYINDKITLQTKFQN---TVETIGEGKDLTYGSFGYIEYSTTIQFPDEH---PKI	613
cry8Aa	FEFTLYLG-DTIEKNRFN-----KTMNGASLTETFKFASFITDFQFRETQ---DKI	638
cry10Aa	KTTVFLTIGIDTISVELPS----TTSRQNPATDLTYADFGYVTFPRTPVKNKTFEGEDTLL	626
cry16Aa	SKLILRKWKGEYIQQQI-----HNISPTYGAFSYLESTITTTTENIFDLTME-VTPY	626
cry19Ba	GQMMINIGYQNPTYFNII-----PTTSRDYTELK-FEDFQLVDTSYIYSGGPS-ISS--	614
cry24Aa	CQFLMKRWPSTGVAPRQWAR---HNVQGTFSNSMRYEAFKYLDIFTITPEENN-----	626

Fig. 1D

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axmi007	IFNRADVSN-SILIIDKIEFIPITSSVRQNREKQKLETIQTKINTFFTNHTKNTLNIEAT	739
cry1Aa	TLSAHVFNSGNEVYIDRIEFVPAEVTFEA---EYDLERAQKAVNELFTSSNQIGLKT DVT	640
cry1Ac	IVGVNRFSGTAGVIIDRFEFIPVTATLEA---EYNLERAQKAVNALFTSTNQLGLKTNVT	642
cry1Ia	TIGAWNFSGNEVYIDRIEFVPVEVTYEA---EYDFEKAQEKVTALFTSTNPRGLKTDVK	677
cry3Aa1	QIGVTGLSAGDKVYIDKIEFIPVN-----	652
cry3Ba	IIGAESFVSNEKIYIDKIEFIPVQ-----	659
cry4Aa	VFNRSDVYTNTTVLIDKIEFLPITRSIREDREKQKLETVQOIINTFYANPIKNTLQSELT	714
cry6Aa	-----	---
cry7Aa	TLHLSDLNNSFFYVDSIEFIPVDVNYAE---KEKLEKAQKAVNTLFTE-GRNALQKDVT	669
cry8Aa	LLSMGDFSSGQEVYIDRIEFIPVDETYEA---EQDLEAAKKAVNALFTNTKD-GLRPGVT	694
cry10Aa	MTLYGTPNHSYNIYIDKIEFIPITQSVLDYTEKQNIKTQKIVNDLFDVN-----	675
cry16Aa	GRQFVEDIPS--LILDKIEFLPTN-----	648
cry19Ba	NTLWLDNFSNGPVIIDKIEFIPLGITLNQAQGYDTYDQNGMYHQNYNSNGYNYNQEYN	674
cry24Aa	-AFTIDLES GGDLFIDKIEFIPVSGSAFEYEGKQNIKTQKAVNDLFIN-----	674
axmi007	NYDID-----	744
cry1Aa	DYHIDQVSNLVECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWR	700
cry1Ac	DYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWG	702
cry1Ia	DYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM-----	719
cry3Aa1	-----	---
cry3Ba	-----	---
cry4Aa	DYDIDQAANLVECI SEELYPKEKM LLLDEVKNQKLSQSRNVLQNGDFE---SATLGWT	770
cry6Aa	-----	---
cry7Aa	DYKVDQVSILVDCISGDLYPNEKRELQNLVKYAKRLSYSRNLLDPTFDSINSSEENGWY	729
cry8Aa	DYEVNQAANLVECLSDDLYPNEKRLLFDVREAKRLSGARNLLQDPDFQEING--ENGWA	752
cry10Aa	-----	---
cry16Aa	-----	---
cry19Ba	TTYQSYNN-----	682
cry24Aa	-----	---

Fig. 1E